Appendix A

>Top sequence C5aR human >Bottom sequence C5aR mouse						350 aa vs. 347 aa
65.6% identity overall N-terminal and 2^{nd} extracellular loop are underlined, 29.0% identity						
C5aP human	1 MNGENVEED			30	40 50	CMT CMAT MA
C5aR human MNSFNYTTPDYGHYDDKDTLDLNTPVDKTSNTLRVP-D ILALVIFAVVFLVGVLGNALVV ::: : : : : : : : : : : : : : : :						
C5aR mouse			[MDPNIPADG		DVAALIIYSVVFLV 40 50	
	60	70	80	90	100 110	
C5aR human	WVTAFEAKR			ALPILFTSIV	OHHHWPFGGAACS	ILPSLILLN
C5aR mouse					NHNYWYFDATACI	
Court mouse	60	70	80	90	100	110
	00	70	00	70	100	110
1	20 1	20 1	1.40	1.50	160 170	
				150		
Coak numan			_		CAVAWGLALLLTIP	
					.::: :::::::	
C5aR mouse	MYASILLLA	ΓISADRFLLV			GVAWVLALLLTIP	SFVYREAYK
	120	130	140	150	160	170
1	80 1	90	200	210	220 23	0
C5aR human	EYFPPKVLC	GVDYSHDKR-	-RERAVAIVE	LVLGFLWPLI	TLTICYTFILLRT	WSRRATRST
					::.:::::	
C5aR mouse					TLNICYTFLLLRT	
Coar mouse	180	190	200	210	220	230
	100	190	200	210	220	230
	0.4.0	252	0.60	070	000	0
	240			270		-
C5aR human	KTLKVVVAV	VASFFIFWLE	PYQVTGIMMS	FLEPSSPTFI	LLNKLDSLCVSFA	YINCCINPI
	::::::::	: ::::::	::::::	.: :::::.	::.::::::::	:::::::
C5aR mouse	KTLKVVMAV	VICFFIFWLE	PYQVTGVMIA	WLPPSSPTL	KRVEKLNSLCVSLA	YINCCVNPI
	240	250	260	270	280	290
	300	310	320	330	340 35	0
C5aR human	TYVVAGOGE	OGRIJRKSIJPS	STITRNVTITEF	SVVRESKSFI	RSTVDTMAOKTOA	V
C5aR human IYVVAGQGFQGRLRKSLPSLLRNVLTEESVVRESKSFTRSTVDTMAQKTQAV						
C5aP moura					PSTDDTSPRKSQA	
CJan Mouse	_			330	-	v
	300	310	320	330	340	